Probe

Newsletter for the USDA Plant Genome Research Program

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Arabidopsis Database Nears Completion

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A specialized genome database on the small plant *Arabidopsis thaliana* is expected to be available this spring to assist molecular biologists, geneticists, and other researchers. Scientists at the Massachusetts General Hospital (MGH) in Boston developed the database, known as AATDB (An *Arabidopsis thaliana* Database).

The database is one objective of the Multinational Coordinated *Arabidopsis thaliana* Genome Research Project. It was initiated primarily to encourage a coordinated research effort to use *Arabidopsis* as a model system for studying the biology of flowering plants.

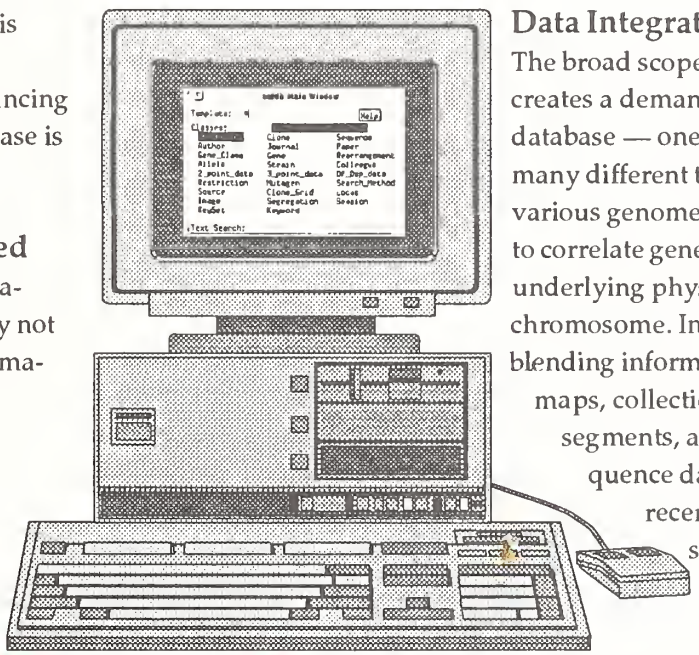
The *Arabidopsis* genome project has reached the point where the physical map is taking form. Because the genome of *Arabidopsis* is small, about 1/30th the size of the human genome, the project is advancing rapidly. Thus, the need for a database is acute.

Specialized Database Needed

Why the need for a specialized database? Existing databases are simply not adequate to manage genomic information in a useful way. Molecular biologists and geneticists routinely use computers and databases to organize and interpret complex biological information; however, these databases are typically intended to perform a single set of related tasks and present the results of a query on the computer screen as text.

For example, one database may retrieve and analyze DNA sequences, while another offers bibliographic information, and still another tracks down the availability of mutant strains.

This segregation by data type may seem to be an efficient way to manage information. However, the specific focus of the "divide and conquer" strategy is not without cost — the user who needs to follow an information trail through several databases will find the experience awkward and frustrating.



Data Integration

The broad scope of the genome initiative creates a demand for a new kind of database — one that accommodates many different types of information. The various genome projects' intentions are to correlate genetic information with the underlying physical structure of the chromosome. In effect, this means blending information — such as genetic maps, collections of cloned DNA segments, and DNA/protein sequence databases — that, until recently, was maintained separately.

As thousands of overlapping cloned

DNA segments are matched with each other and aligned into large, continuous "physical maps," the need to integrate the data in a practical way becomes necessary for bookkeeping purposes and for the convenience of access. Management of a large-scale combined cloning and DNA sequencing effort requires that it be possible to visualize at a glance the relationships between cloned DNA segments, the genetic map, and the DNA sequence database. The overall status of the project can then be monitored. Ultimately the information recipients — the greater scientific community — need the same tools if they are to use the information effectively.

AATDB Design

AATDB is designed along the broadly-inclusive principles described earlier. The database allows a researcher to browse the enormous variety of information associated with the *Arabidopsis* genome and zero in on specific details. The process is simplified by using graphics. Genetic maps, physical maps, and the features of DNA sequences are drawn as pictures in the way that molecular biologists are accustomed to seeing them, rather than presented as columns of text and numbers.

The *Arabidopsis* database goes well beyond the "single purpose" biological databases most scientists are accustomed to using today because of two important features. First, users obtain information from the database by using a mouse to "click on" objects in windows, in much the same way the Apple Macintosh computer allows the user to retrieve information. Information in AATDB is always available in windows, whether it is simple text (for example, a bibliographic reference) or a pictorial representation of something more abstract (such as a genetic or physical map). In either case, users find out more information or move to completely new categories of information by "clicking on" hot spots, which can be either words or symbols.

Second, information in the database is linked together by a large number of interconnections. There is no single starting point for asking a question, nor are users required to move through the information in a single direction along a single path. Consequently, specific information in the database can be found in a variety of ways.

AATDB also features a query language that can be used to directly search for key words, phrases, or values in specific fields.

Central Feature

The central feature of AATDB is the integrated presentation of the genetic map, the physical map, and the DNA sequences that have been determined for *Arabidopsis*. The genetic map consists of over 500 markers on 5 chromosomes; the physical map currently contains nearly 15,000 cloned DNA segments. The DNA sequence collection contains over 300 entries from the GenBank DNA database, including their annotation. For each DNA sequence, the results of "similarity searches" are also available (obtained by comparing all possible amino acid translation products for each DNA against several protein sequence databases).

In addition to the genetic and physical maps, AATDB contains bibliographic references for journal articles, books, theses, and symposia, which are organized by author, journal, and accession number. Many references have been provided by the National Agricultural Library (NAL) from the AGRICOLA bibliographic database as well as from other

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sources. Information for strains from the Nottingham Stock Centre Seed Catalog has been provided by the Stock Center at Nottingham, England. Also included are the contents of "The Greenbook" for *Arabidopsis* by Meyerowitz and Pruitt (with gene, allele, and bibliographic entries cross-referenced to the rest of the database). In addition, the database includes contact information for over 350 researchers and segregation data for many RFLP markers.

Plans are to add more information, including scanned images, to document both the characteristics of mutant strains and the hybridization patterns produced by RFLP probes; an expanded list of keywords; raw data from genetic crosses; information on characteristics of mutant alleles; all seed, stock, and clone information from the new Ohio State University/Michigan State University *Arabidopsis* Biological Resource Center; and other information pertinent to the *Arabidopsis* community.

Database Software

The software for the database came from Dr. Richard Durbin (MRC, Cambridge, UK) and Dr. Jean Thierry-Mieg (CNRS-CRBM, Montpellier, France). Last year they released a database to accommodate the rapidly accumulating information generated by the *C. elegans* genome project. An important feature of the *C. elegans* database, called ACEDB (A *Caenorhabditis elegans* Database), is that it is easily adapted to meet the informatic requirements of a wide variety of organisms. This versatility makes it relatively easy to reconfigure ACEDB to manage information for *Arabidopsis thaliana*.

Obtaining AATDB

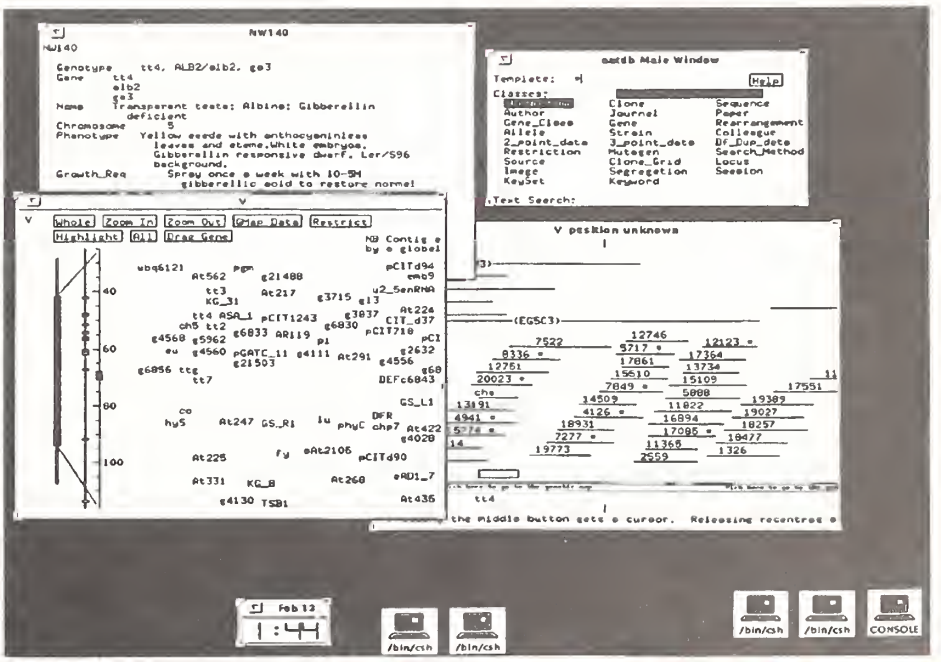
The database currently runs as a stand-alone system on Sun Microsystems work stations as an X-Windows application. Plans are to make available an Apple Macintosh version. Currently, Macintosh and Microsoft Windows users, or individuals with access to X-Windows server software, can use AATDB via a network connection to a UNIX computer that runs the database software.

AATDB is a stand-alone distributed, rather than a centralized, database. To obtain AATDB, users will copy the database software and data from an archive on the Internet worldwide computer network. Once the local copy of AATDB is installed, users can run the software on their work stations and have access to all the collective *Arabidopsis* information. Initially, the database will be distributed via Internet anonymous FTP procedure from sites in the United States, including NAL and MGH. Distribution sites will also be established overseas. Electronic mail and the same FTP mechanism will be used to distribute updates to the software and data. Eventually, a CD-ROM version will be available from NAL.

The USDA Plant Genome Research Program is providing funding through NAL to support the database development for *Arabidopsis thaliana* and four additional plant species: wheat, pine, soybean, and maize. Eventually the information from the five databases will be fed into a main database at NAL.

Contact

Readers who desire additional information about AATDB can contact Dr. Sam Cartinhour or Dr. J. Michael Cherry in Professor Howard Goodman's laboratory via Internet computer mail at curator@frodo.mgh.harvard.edu, or via FAX (617) 726-6893. ◆



Competitive Edge

Plant Genome Research Grant Program First Annual Report - 1991

Dr. Susan McCarthy, Coordinator
Plant Genome Data and Information Center
National Agricultural Library, USDA
Beltsville, MD

USDA's 1992 Plant Genome Grants Program is well underway. Proposals submitted are now in the review process. The following is a summary of the 1991 program results.

The Plant Systems Division of the National Research Initiative Competitive Grants Program (NRICGP) in USDA's Cooperative State Research Service administers the plant genome grants. In 1991, the bulk of plant genome funds went to support awards made in two programs in the Plant Systems Division: The Plant Genome Program and the Plant Genetic Mechanisms and Molecular Biology Program. Plant genome funds also supported some awards in the Division's remaining five programs. While the projects that were funded cover a diversity of topics, all are directed toward advancing the understanding of plant genetic structure and mechanisms.

In all, 1991 plant genome funds — totalling $10.5 million — currently support 77 research projects. The funds also have supported one conference. Over 250 applicants competed for the grants. A list of awardees and their research topics is included in this issue.

Nearly 90 percent of the awards were for projects on the agronomic crop species. Table 1 provides a breakdown by plant species, and depicts the number of individual awards, total money awarded, and percentage of the total.

Figure 1

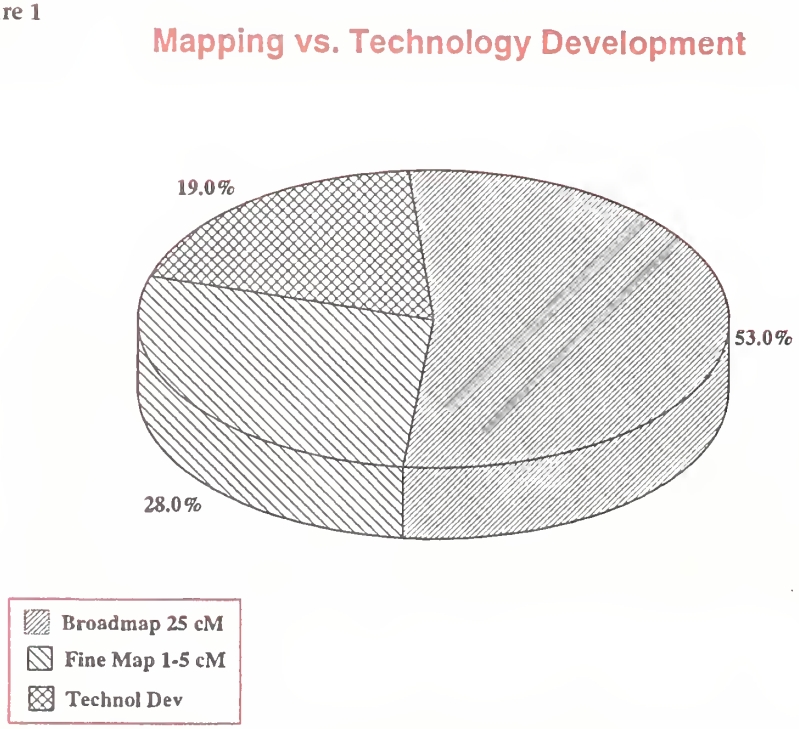


Table 1

Species, Number of Grants, and Funding Level

Species	Number of Grants	Grant Amount	Percentage of Grant Total
Corn	21	$ 2,642,000	25
Tomato	13	2,387,000	23
Bean	4	270,000	3
Cotton	2	260,000	2
Soybean	3	306,000	3
Wheat	2	176,000	2
Sorghum	1	210,000	2
Barley	1	120,000	1
Alfalfa	3	437,151	4
Pea	2	325,000	3
Cabbage	1	180,000	2
Potatoe	1	180,000	2
Rice	1	60,000	1
Pepper	1	260,000	2
Brassica	4	318,374	3
Lettuce	1	265,000	3
Poplar	2	250,000	2
Flax	1	150,000	1
Cuphea	1	210,000	2
Carrot	1	118,000	1
Tobacco	2	275,000	3
Pine	3	260,000	2
Chlaymodomonas	1	185,000	2
Arabidopsis	7	885,000	8
Cyanophora	1	150,000	1
Total	76	$ 10,489,525	104

Note: The total number of grants is 76. The total dollar amount is $10,498,525. The difference between the total values is due to more than one species reported per grant. Average per grant is $138,020.

Of the plant genome awards, 64 percent were unidisciplinary projects while 36 percent were multidisciplinary. Overall for NRICGP, multidisciplinary awards averaged 28 percent of the total. Mission-linked grants accounted for 26 percent of the total 1991 program.

Figure 1 shows the plant genome grants breakdown for mapping and technology development. Broad- or low- resolution mapping for the less well defined species accounted for 53 percent of the 1991 awards.

In terms of gene systems or traits, 76 NRI grants were given in the following areas: Insect resistance, nematode resistance, disease resistance, yield (QTL's), ripening, floral traits, triacylglycerols, and technology development. ◆

Grant recipients ☞

Marcus Rhoades Memorial Fund

Marcus Rhodes, one of the world's distinguished maize geneticists, died December 30, 1991. A fund in Rhoades' memory has been set up at Indiana University to financially assist graduate students there. Individuals who would like to make a donation in Rhoades' memory of can send a check to Tom Blumenthal, Chairman, Department of Biology, Indiana University, Bloomington, IN 47405. Please make the check payable to the I.U. Foundation - Marcus Rhoades Memorial Fund.

The Class of 1991 Plant Genome Grant Recipients

Jane Aldrich
Case Western Reserve University
Isolation of Rust Resistance Genes in Flax

David Altman
USDA / ARS Southern Crops Research Laboratory
Glanding-Control Genes of Cotton: A Model System for Gene Expression

Frederick Ausubel
Massachusetts General Hospital
Use of Genomic Substraction for Cloning Plant Genes

Barbara Baker
USDA / ARS Plant Gene Expression Center
Ac and Ds Transposon-Based Genetic Tools for Tomato

Jeffrey Bennetzen
Purdue University
Molecular Genetic Analysis of Rpl-Mediated Disease Resistance in Maize

Jeffrey Bennetzen
Purdue University
Parallel Studies of Genome Organization in Maize and Sorghum

Edwin Bingham
University of Wisconsin - Madison
Defining Gene Action for Yield in Autotetraploid Alfalfa

James Birchler
University of Missouri-Columbia
Chromosomal Manipulation in Maize

David Bisaro
Ohio State University
Molecular Mechanisms of Geminivirus Replication

Lawrence Bogorad
Harvard University
Functional Features of the Chloroplast Genome

Hans Bohnert
University of Arizona
The Cyanelle Genome - An Evolutionary Legacy of Plant Genes

Harvey Bradshaw
University of Washington
Low-Density Genetic Mapping in Populus Genome

Roxanne Broadway
Cornell University
Defensive Efficacy and Molecular Characterization of Cabbage Trypsin Inhibitor

Gordon Cannon
University of Southern Mississippi
Biochemical Characterization of Soybean Chloroplast DNA Replication in Vitro

John Carman
Utah State University
Embryogenic Tissue Cultures of Wheat: Production, Transformation and Regeneration

Christine Chase
University of Florida
Molecular Genetics of Fertility Restoration in CMS

Joanne Chory
The Salk Institute for Biological Studies
Molecular and Genetic Analysis of Arabidopsis DET2 Gene

Prem Chourey
University of Florida
Analysis of Minature and the Two Sucrose Synthase Genes in Maize

Gary Churchill
Cornell University
Converting RFLP Linkage Maps into Physical Maps: Theory and an Application

Michael Devey
USDA Forest Service
RAPD Linkage with a Major Gene for Blister Rust Resistance in Sugar Pine

Rebecca Dickstein
Drexel University
Nodule Morphogensis Genes of Medicago

Robert Ferl
University of Florida
Chromatin Structure and Gene Expression in Plants

Bikram Gill
Kansas State University
Molecular Cytogenetic Analysis in Wheat

Wilhelm Gruissem
University of California - Berkeley
Regulation of Tomato Fruit Development and Differentiation by HMG CoA Reductase

Tim Helentjaris
University of Arizona
High Density Genetic Map for Maize Including Molecular and Phenotypic Loci

Thomas Hodges
Purdue University
Homologous Recombination Between DNA Molecules in Plant Cells

Margaret Hoey
University of Georgia
A Complete Genetic Map for Liriodendron (Yellow Poplar)

Stephen Howell
Boyce Thompson Institute for Plant Research, Inc.
Isolation of Genes Involved in Cytokinin Responses in Arabidopsis

Anthony Huang
University of California - Riverside
Molecular and Cell Biology of Oil Bodies in Maize and Brassica

Keith Hutchison
University of Maine
A Molecular Genetic Linkage Map for Conifers

Noel Keen
University of California - Riverside
Cloning and Mapping of Soybean Genes for Disease Resistance and Other Characters

Jerry Kermicle
University of Wisconsin - Madison
Transposition of Ac/Ds Mobile Elements in Maize

Steven Knapp
Oregon State University
A Genetic Map of Cuphea: Fatty Acid Synthesis Loci and Transposable Elements

Molly Kyle
Cornell University
Genomic Mapping and the Transfer of Broad Spectrum Plant Virus Resistance

Christopher Lamb
Salk Institute for Biological Studies
Gene Activation Mechanisms in the Initiation of Plant Defense Responses

Brian Larkins
University of Arizona
Third International Congress of Plant Molecular Biology

Robert Martienssen
Cold Spring Harbor Laboratory
Molecular Analysis of the Iojap Gene in Maize

Douglas Maxwell
University of Wisconsin - Madison
Trans-Dominant Interference as a Mechanism for Resistance to Plant Geminiviruses

Stephan Mayfield
Research Institute of Scripps Clinic
Nuclear and Chloroplast Gene Interactions Regulating Expression of Photosystem II Proteins

Donald McCarty
University of Florida
Viviparous-1 Mediated Repression of Alpha Amylase Genes in Maize Aleurone

Shiela McCormick
USDA/ARS/PWA
Constructing and Characterizing a Tomato YAC Library to Clone Male Sterile Genes

Thomas McCoy
Montana State University
Use of Molecular Markers to Study Recombination and Heterosis in Alfalfa

Richard Michelmore
University of California - Davis
A Genetic Map of *Lactuca sativa* with Sequence Characterized Amplified Regions

Michael Mulligan
University of California - Irvine
RNA Editing in Maize Mitochondria

Martha Mutschler
Cornell University
Genomic Regions Associated with Acylsugar Biosynthesis and Insect Resistance

June Nasrallah
Cornell University
Molecular Analysis of the Cellular Interactions of Incompatibility in Brassica

Myron Neuffer
University of Missouri
Selection Characterization and Preservation of Maize Mutants

Brent Nielsen
Auburn University
Localization and Characterization of Chloroplast DNA Replication Origins

Suzanne Nielsen
Purdue University
Molecular Cloning of Soybean Cysteine Proteinase Inhibitors for Insect Resistance

Mary O'Connell
New Mexico State University
A Mitochondrial Mutation in Tomato Alters Vegetative and Reproductive Growth

Thomas Osborn
University of Wisconsin - Madison
Cytoplasmic Effects on Genome Stabilization in Brassica amphidiploids

David Ow
USDA/ARS
Generating Site-Specific Chromosomal Deletions and the Cloning of Deletions Loci

Andrew Peterson
Texas A&M University
Molecular Mapping of the Cotton Genome Using DNA Markers

Peter Peterson
Iowa State University
Transposon Tagging of Agriculturally Important Disease-Resistant Genes in Maize

Ronald Phillips
University of Minnesota
Molecular and Genetic Analysis of Tissue Culture-Induced Variation

Robert Plaisted
Cornell University
Potato RFLP Map to Introgress Insect Resistance From Wild Species

Charles Rick
University of California - Davis
Analysis of the Tomato Genome via Lycopersicon x Solanum Hybrids

Donald Robertson
Iowa State University
Isolation of Genes for Quantitative Inheritance in Maize

Ronald Sederoff
North Carolina State University
Molecular Markers to Accelerate Breeding in Loblolly Pine

Phillip Simon
USDA/ARS/Midwest Area
Molecular Markers for a Low-Resolution Genetic Map of Carrot

Karambir Singh
University of California - Los Angeles
Analysis of OCS-Element Enhancer Sequences in Arabidopsis

James Smith
Texas A&M University
Development of Molecular Probes to Augment Breeding for Quality Protein Maize

Shauna Somerville
Michigan State University
Identificaiton of Molecular Markers Adjacent to the M1-a Locus in Barley

David Speiser
USDA/ARS/Plant Gene Expression Center
Characterization of Genes for Phytochelatin Biosynthesis in *Brassica juncea*

Steven Spiker
North Carolina State University
Plant Nuclear Scaffolds: Structural and Functional Analysis

Robert Spreitzer
University of Nebraska
Chloroplast Heteroplasmic Suppression

John Steffens
Cornell University
Function and Expression of Polyphenol Oxidase

David Stern
Boyce Thompson Institute for Plant Research, Inc.
***In vitro* Analysis of Plant Mitochondrial Transcription**

Donald Strauss
Brandeis University
Use of Genomic Substraction for Cloning Plant Genes

Thomas Sullivan
University of Wisconsin - Madison
Molecular and Biochemical Analysis of the Maize Brittle-1 Gene

Steven Tanksley
Cornell University
Development of Map-Based Cloning in Crop Plants: Tomato as a Model System

Norman Weedson
Cornell University
Mapping, Host Genes Affecting Plant-Microbe Interactions in Temperate Legumes

Valerie Williamson
University of California - Davis
Molecular Characterization of the Nematode Resistance Locus of Tomato

Rod Wing
Texas A&M University
Development of Map-Based Cloning in Crop Plants: Tomato as a Model System

Ray Wu
Cornell University
Isolation of Chromosome-Sized DNA and Construction of a Physical Map

Gracia Zabala
University of Illinois
Characterization of Cytoplasmic Reversion & Nuclear Restoration in Maize ◆

Other Pursuits

Canada's Wheat Genome Mapping Efforts

Dr. W. K. Kim and Dr. T. F. Townley-Smith
Agriculture Canada Research Station-Winnipeg
Manitoba, Canada

Canadian researchers have increased their networking capability and strengthened communication with each other as a result of establishing the Canada Wheat Genome Mapping Group.

The scientists formed the Group in Winnipeg in February 1990 when the RFLP Workshop-Agriculture Canada BioCrop Network convened in conjunction with the Canada Expert Committee on Plant Breeding and Plant Disease. At the discussion session of the Cereals RFLP Syndicate, participants selected two coordinators for the Group, Drs. Won K. Kim and N. K. Howes of the Agriculture Canada Winnipeg Research Station.

Rather than initiate wheat RFLP mapping immediately, the Group decided to focus on the application of the technology (for example, the use of PCR and barley probes to wheat; support of barley initiatives of the North America Barley Genome Mapping Project; and the use of available probes to tag smut and bunt resistance, and high protein genes).

Group Membership

Currently, there are 34 individual members with the following interests: RFLP Mapping, 6; Cytogenetics (includes *in situ* hybridization and development of double-haploids), 5; Genetic Analysis and Field Tests (agronomic and disease evaluation), 19; Molecular Biology, 2; and Quality Tests, 2.

Canadian research establishments that have a cereal biotechnology program on-site are involved in the mapping effort. Participating institutions are: The Plant Research Centre, Agriculture Canada, Ottawa; the Winnipeg Research Station; the Lethbridge Research Station; the University of Guelph; and the University of Saskatchewan. Some members of these establishments serve on the recently organized Steering Committee.

In February the Group held a Genome Mapping Workshop in Saskatoon, Saskatchewan, at the Canada Expert Committee meeting. Once the Group's mandate and genetic resources are identified for the mapping effort, more research institutions are expected to participate.

Winnipeg's RFLP Analysis

One project of the Winnipeg Research Station is the RFLP analysis of wheat and barley genomes. Coordinated by Dr. Kim and Dr. T. F. Townley-Smith, the project's objective is to identify genes for rust, smut, and sprouting resistance. These are the integral components of the Station's cereal cultivar development program.

RAPD (random amplified polymorphic DNA) primers (arbitrary nucleotide sequence) are now widely used to amplify the genomic DNA by PCR and to detect polymorphism among cereal cultivars. These findings can be used as genetic markers and to construct genetic maps. Researchers are in the process of screening 400 RAPD primers that were synthesized by the University of British Columbia Biotechnology Centre staff. Of 150 screened, researchers found 41 polymorphic primers in barley and 35 in wheat. The following cereal cultivars are

used for the genetic analysis with selected RAPD markers:

Barley (in collaboration with Dr. P.L. Thomas) — Researchers use Hannchen (2 row) with covered smut resistance gene and Plush (6 row) with covered smut resistance gene. (These two genes are not linked.) Nineteen RAPD markers are in analysis, using F6 recombinant inbred lines. Sixty of 100 single seed descent lines were screened for disease reaction.

Wheat (in collaboration with Dr. N.K. Howes and Mr. R. Knox) — Researchers are interested in tagging a bunt resistance gene and a sprouting resistance gene. A wheat germplasm RL 4555 (soft, white, sprouting resistance gene) x Biggar BSR (bunt resistance gene bt-10 (derived from BW553)) and smut resistance gene (derived from Glenlea). We have F3 single seed descent lines for analysis, using 15 RAPD markers.

Wheat (in collaboration with Mr. E. Czarnecki) — Researchers are interested in mapping a bunt resistance gene and finding DNA markers that would detect polymorphism. Wheat cultivar Roblin x BW 553, BC3 F2, and BC3 F5 are now available for RAPD analysis. Researchers also found polymorphism between these materials when ribosomal DNA repeat unit was restricted with Bam H1 and probed with pMF2 (ribosomal RNA genes of *Neurospora crassa*).

For cereal DNA analysis at the Station, researchers identified several useful parental lines: RL 4555 (soft, white, sprouting resistance gene); Biggar BSR (bt 10, bunt resistance gene and smut resistance gene); Chinese Spring Sr 6 (stem rust resistance gene); BW 121 (streak mosaic virus resistance gene); Timgalen (Australian germplasm, stem rust resistance genes, Sr 5, Sr 6, Sr 8, Sr Tt), and Sr T (Australian wheat cultivars by CSIRO, 1975). The mapping populations would include single seed descent and double-haploids.

Related Research

Other related research includes Ribosomal DNA repeat unit polymorphism in 27 accessions of six species of *Aegilops* (in collaboration with Dr. E. R. Kerber and Mr. B. Innes). Species of the genus *Aegilops* are important sources of useful alien genes in developing wheat cultivars with disease and insect resistance, and cold hardiness. In an effort to understand the genetic diversity amony several species, the ribosomal RNA genes were double-digested with Bam HI and Eco RI. Researchers found that two accessions of *Ae.squarrosa var.strangulata* (collected from Turkmenia and Azerbaijan, former USSR) had two additional Bam HI sites in the non-transcribed spacer region in addition to two sites in the coded regions.

Contact for Information

For more information on the Canada Wheat Genome Mapping Group and the genetic material currently under investigation, please write to Dr. Won K. Kim, Agriculture Canada Research Station, Winnipeg, Manitoba, Canada R3T2M9; Ph. (204) 983-5533 or 983-2340; FAX (204) 983-4604. ◆

Ag NewsFAX

WASHINGTON — The U.S. Department of Agriculture has expanded its Ag NewsFAX service to include fact sheets on USDA's agencies and programs, and biographical information on top USDA officials.

Ag NewsFAX lets news media select specific USDA news materials and receive them immediately on their fax machines. It operates 24 hours a day, 7 days a week. USDA news releases have been available on Ag NewsFAX for several months. Summaries of Outlook and Situation Reports from USDA's Economic Research Service were added in August.

To try Ag NewsFAX, use a touchtone telephone connected to a fax machine, dial (202) 690-3944 and follow the voice prompts. Or for detailed instructions, as soon as the system answers push 9 on the telephone, and hit the start button on the fax machine. Information on using Ag NewsFAX will be faxed to you.

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Sources

Triticeae Gene-Mapping Scientists Unite

Dr. Harold Corke and Dr. Patrick E. McGuire
ITMI Management Office
Genetic Resources Conservation Program
University of California, Davis, CA

Wheat, barley, rye, and triticale — all members of the grass tribe Triticeae — have contributed immensely to human development and continue to dominate much of world agriculture.

Many wild related species in the same tribe are a fruitful source of alien genetic material that can be used to improve modern cultivars and enhance their genetic base. The transfer of alien genes or chromosome segments conferring economically important traits, such as disease resistance or quality, is aided by knowledge of the chromosomal location, or genetic map position, of the trait.

International Coordination Initiative

Scientists around the world are working to develop comparative genetic maps of various Triticeae species utilizing restriction fragment length polymorphisms (RFLPs) and other markers. The need to coordinate and strengthen international efforts on genome mapping of wheat and related species provided the impetus to develop the International Triticeae Mapping Initiative (ITMI) in 1988. Individuals credited with developing the concept are Jan Dvorak and Cal Qualset (University of California, Davis), Gary Hart (Texas A&M University), and Bikram Gill (Kansas State University).

The goal of ITMI is to reduce the repetition of similar work by participants, thereby maximizing the rate of progress in research efforts.In June 1989, at a workshop held in Davis, California, a small group of individuals clarified the aims of ITMI as follows:

Participants of the 1991 ITMI Public Workshop in Manhattan, Kansas, included (from left) Bikram Gill (KSU), Steve Graham (Kansas Wheat Commission), Dick Stuckey (National Association of Wheat Growers Foundation), and Cal Qualset (UC-Davis). (Photo by Harold Corke)

1) To develop linkage and metaphase chromosome maps utilizing RFLP markers of the chromosomes of durum wheat (*Triticum turgidum*) and common wheat (*T. aestivum*).
2) To develop a comparative map of barley (*Hordeum vulgare*) utilizing RFLP markers.
3) To develop a comparative map of rye (*Secale cereale*) utilizing RFLP markers.
4) To develop comparative maps of representative diploid species of the genera in the Triticeae.
5) To construct comparative linkage maps of the diploid ancestors of the wheat A, B, and D genomes.
6) To determine linkage between RFLP markers and genes controlling specific agronomically important traits.

ITMI Coordinators

ITMI is coordinated at the University of California, Davis, by Calvin Qualset. ITMI coordinators, listed below, are responsible for coordinating a particular chromosome group in wheat, mapping efforts in another related species, or other related functions (such as database development):

- Olin Anderson (USDA / ARS, Albany, California)
- Rudi Appels (CSIRO, Canberra)
- Jan Dvorak; Michael Gale (Cambridge Laboratory, Norwich, England)
- Bikram Gill; Perry Gustafson (USDA / ARS, University of Missouri)
- Gary Hart; David Hoisington (CIMMYT, Mexico)
- Rafiqul Islam; Peter Langridge; Ken Shepherd (University of Adelaide)
- Peter Sharp (University of Sydney)
- Mark Sorrells; Steven Tanksley (Cornell University)

Annual Workshops

An annual public workshop provides a forum for presenting research results andexchanging ideas. Workshop participants include ITMI coordinators, ITMI investigators (scientists who are working on any relevant area of cereal genetics), and ITMI affiliate members (representatives of institutional supporters of ITMI). Proceedings of the sessions are published. Planning is underway for the third annual workshop to be hosted by CIMMYT in Mexico this September. ITMI participants held their first workshop in 1990 in Sacramento, California. A second workshop followed in Manhattan, Kansas, in 1991.

A special feature of ITMI is the wide international participation in this field of research and at the meetings. Genome mapping is an exciting area of modern plant genetics with many potential applications in crop improvement. Rapid progress is evident. As an example, some maps presented at the meetings doubled in the number of mapped probes between 1990 and 1991.

Facilitating Information Exchange

ITMI emphasizes the free exchange of information, materials, probes, and genetic stocks. As mapping progress advances, masses of data accumulate. Thus, the communication role of ITMI has become increasingly important in facilitating information flow.

The USDA Plant Genome Research Program recognizes the importance of computer database development in making genome mapping results available to researchers. Agricultural Research Service Scientist Olin Anderson is leading the efforts of USDA's wheat database project in collaboration with programmers at the Lawrence Berkeley Laboratory (LBL) and staff of USDA's National Agricultural Library.

At a meeting of the wheat database group, held prior to the 1991 ITMI Public Workshop in Kansas, John McCarthy (LBL) provided a demonstration of a prototype database that included a user-friendly graphic interface. Wheat researchers then had the opportunity to discuss their needs and expectations of the database.

The ITMI Management Office also functions as an information resource. With financial support from the USDA program, staff are developing an ITMI newsletter.

Additional Information

Further information about ITMI may be obtained from the ITMI Management Office, Genetic Resources Conservation Program, University of California, Davis, CA 95616 USA; Phone (916) 757-8920; FAX (916) 757-8755. ◆

From the Hill

The Federal Biotechnology Commitment

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Biotechnology is on the move. The industry is rapidly expanding, with approximately 1,100 companies in the United States alone engaged in some aspect of biotechnology. Most of the companies are small — 76 percent have 50 or fewer employees. Revenues in 1991 amounted to about $4 billion in product sales. Human therapeutics have the greatest market share (35 percent). Agricultural biotechnology accounts for 8 percent of biotechnology markets.

Government Support

The Federal Government has recognized the importance of biotechnology in developing new jobs and products. Congress and the President are working to foster the industry. A Presidential Initiative is in the works for FY 1993. The President's FY 1993 budget targets $4.03 billion for biotechnology research, a 7 percent increase over the FY 1992 budget. The bulk of the money will be spent on biomedical research. Agricultural biotechnology would receive about $207 million. A detailed report of the Bush initiative is available. To obtain a copy, see the screened box.

Another project underway in the Federal arena is the National Technology Initiative which was launched by President Bush last February. Its goal is to promote a better understanding of the opportunities for industry to commercialize new technology advances. To help implement this initiative, thousands of firms have been meeting with Federal representatives at 11 conferences held around the country. Agricultural biotechnology and the transfer of this new technology is one of the key program areas discussed at three of these meetings.

In Congress, House and Senate members have come together in a bipartisan coalition to form the Congressional Biotechnology Caucus. Their purpose is to provide an informal forum to promote and support the biotechnology industry. Senate Co-chairs are Frank Lautenberg (D-NJ) and Hank Brown (R-CO). House Co-chairs are Tom McMillen (D-MD) and Tom Bliley (R-VA).

Caucus Issues

Issues to be addressed by the Caucus include:

- Broadening the support and knowledge of biotechnology advances and benefits.
- Developing awareness of and addressing solutions for the problems of the biotechnology industry.
- Increasing awareness of the economic benefits the United States receives from the biotechnology industry.

Biotechnology Report Available

The report describing the Presidential Initiative on biotechnology is available for purchase. To obtain a copy, contact the U.S. Government Printing Office, Superintendent of Documents, Mail Stop: SSOP, Washington, D.C. 20402-9328. Information on the report follows:

Biotechnology for the 21st Century, a report by the FCCSET Committee on Life Sciences and Health
February 1992
125 pp.
ISBN 0-16-036101-X

- Monitoring Administration policy, especially in the area of patents and trademarks.
- Supporting existing committees and members with oversight responsibilities relevant to the biotechnology industry.
- Supporting legislation redressing biotechnology industrial problems and acting as liaison with the Executive Branch.
- Providing an educational forum where ideas and issues involving biotechnology will be exchanged.

The Caucus recognizes the benefits that biotechnology can bring to our society. These benefits include non-toxic biodegradable pesticides, bioremediation of toxic spills, vaccines and treatments for human and animal diseases, and a more productive and nutritious food supply. ◆

The Congressional Biotechnology Caucus

Senate Co-Chairs	Frank Lautenberg (D-NJ) Hank Brown (R-CO)
House Co-Chairs	Tom McMillen (D-MD) Tom Bliley (R-VA)
Staff Contacts	Sander Lurie, Legislative Assistant to Senator Lautenberg (202) 224-6822
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	Mike Simoncic, Legislative Assistant to Rep. McMillen (202) 225-8090
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Biotechnology Caucus business is handled through Rep. Bliley's office.

Off the Wire

Corn Database Aids Research Funding Decisions

Donna Schenck-Hamlin, Coordinator, Food and Feed Grains Institute
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Research funding decisions by private and public sponsors demand increasing information support in the 1990's. To justify the awarding of grants during a period of constrained resources, donors require ample evidence that the proposed work is not redundant, but a logical extension of previous development.

As co-funding between private and public sponsors increases, there is a growing need to capture a profile of research activity in both sectors. This is occurring particularly among commodity associations, that co-sponsor work with government agencies as well as with industry.

These groups' funding decisions are driven by the need for improved market opportunities. Their selection criteria may be more sensitive to changing economic priorities than the strategies of other types of sponsors.

Database Established

A database to support research funding decisions in this environment has been established for the National Corn Growers Association (NCGA) at Kansas State University (KSU). Known as the Corn Utilization Research Database (CURD), the database combines information from public- and private-sponsored research activities in the United States and overseas.

All retrospective research activities funded by NCGA and its associated State checkoff offices are profiled in CURD. Currently, pending research proposals are included as well, so that decision-makers may compare proposals from other States and consider establishing regional funding schemes.

Surveys of patentees and published authors generate additional profiles of expertise in the database that are useful to sponsors who are forming new research teams. A principal source of expertise are participants of NCGA's corn utilization conferences and of other symposia devoted to starch-, protein-, and oil-based field crop products.

The database categorizes research activity with regard to targeted users, the constituents of the plant from which new products are derived, product types, processes, and associated quality issues. Research results are cited from a parallel database, the Postharvest Documentation Service (PHDS), also located at KSU in the Food and Feed Grains Institute.

Challenges

Encompassing the diversity of research on food, feed, and industrial uses for corn is a primary challenge for the database researchers. Another is the inclusion of ongoing private research activity that is rarely disclosed before a product or patent appears. Informal knowledge of such work in commodity associations can be tapped, but citing details other than the expertise of the active workers is problematic.

A database designed for decisionmaking with regard to research requires that connections between recorded activities be made apparent. A current challenge for CURD is the modeling of research progress, as well as the associations

(cont. on page 22 ➤)

Announcing

Plant Genome I

November 9-11, 1992
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Topics

Purpose, Management, and Organization
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Informatics
Beyond the Map
Forest Tree Genome Mapping
Map Generation and Analytical Mapping Software Workshop

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Simple Sequence Repeat DNA Length Polymorphisms

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The suggestion by Botstein et al. (1980) that Restriction Fragment Length Polymorphisms (RFLP) provide the basis of a new type of genetic linkage map has led to the construction of such maps in numerous animal and plant species.

The markers on these maps have had broad application, ranging from the localization of genetic loci controlling human disease to the improvement of plant varieties by plant breeders. While not always the case, RFLP is often the result of the absence or presence of an endonuclease restriction site. Thus, in many instances only two alleles exist at a genetic locus. However, the likelihood that a particular molecular marker locus will be informative is positively related to the number of alleles at that locus. Thus, the probability that two plant inbreds will be polymorphic increases if the possibility of multiple alleles exists. Similarly, in an open-pollinated population the likelihood of heterozygosity at a locus will increase with the number of possible alleles.

The report of RFLP loci in humans with as many as eight different alleles (Wyman and White, 1980) suggested the possibility of greatly enhanced informativeness per locus. These so-called Variable Number Tandem Repeat (VNTR) loci (Nakamura et al. 1987) consist of sets of tandemly repeated DNA core sequences and have been referred to as "minisatellite" sequences by Jeffreys et al. (1985). The core units vary in length from 11 to 60 base pairs and the repeat region is flanked by conserved endonuclease restriction sites. Thus, the length of the restriction fragment produced by this type of genetic locus is proportional to the number of oligonucleotide core units it contains.

To complement RFLP markers, a second type of molecular marker based upon Polymerase Chain Reaction (PCR) technology (Mullis et al., 1986) has recently been widely used in plants. Williams et al. (1990) proposed the use of single arbitrary 10 base oligonucleotide PCR primers for the generation of molecular markers. These Random Amplified Polymorphic DNA (RAPD) markers are easily developed and because they are based on PCR amplification followed by agarose gel electrophoresis are quickly and readily detected. As a result, RAPD's may permit the wider application of molecular maps in plant science. Most RAPD markers are dominant and therefore, heterozygous individuals cannot be distinguished from both homozygotes. This contrasts with RFLP markers which are co-dominant and therefore, distinguish among the heterozygote and homozygotes. Thus, relative to standard RFLP markers, and especially VNTR loci, RAPD markers generate less information per locus examined.

PCR and Repetitive DNA Sequences

Alec Jeffreys and colleagues (Jeffreys et al., 1988) suggested combining the specificity and rapidity of PCR with the informativeness of VNTR loci in humans. Primers to the conserved flanking regions of VNTR loci were developed allowing PCR amplication of an entire VNTR locus. The resulting PCR products possess electrophoretic mobilities that differ according to the number of repeated DNA units in the VNTR allele(s) present.

This approach was recently extended to a different type of repetitive DNA in humans (Litt and Luty, 1989; Weber and May, 1989; Tautz, 1989). Rather than repeat units in the range of 11 to 60 base pairs in length, these workers suggested that high levels of length polymorphism exist in dinucleotide tandem repeat sequences. A dinucleotide repeat such as $(dC\text{-}dA)_n . (dG\text{-}dT)_n$ was reported to occur in the human genome as many as 50,000 times with n varying from 10 to 60. This type of reiterated sequence has been termed a Short Tandem Repeat Edwards et al. (1991), microsatellite (Litt and Luty, 1989) or a Simple Sequence Repeat (SSR) (Jacob, et al., 1991).

As is generally the case with VNTR loci, the DNA sequences flanking SSR's are conserved, allowing the selection of PCR primers that will amplify the intervening SSR in all genotypes of the target species. As initially reported, the PCR reaction includes a small amount of one ^{32}P-labeled nucleotide or one or two ^{32}P end-labeled primers to allow visualization of amplification products via autoradiography after electrophoresis on a standard sequencing gel. Variation in PCR product length is a function of the number of SSR units.

Figure 1 illustrates the detection of SSR length polymorphism using three genotypes, including two inbred parents and their F_1. Parent 1 is homozygous for the $(CA)_n$ allele and Parent 2, the $(CA)_{n-2}$ allele and each produces single PCR products. The F_1, being heterozygous, produces products corresponding to both alleles. Markers resulting from SSR length polymorphisms are placed on genetic maps in relation to other SSR, RFLP, RAPD, and phenotypic markers in a manner identical to that used with RFLP or RADP markers.

Developments

SSR Loci in Humans

Human geneticists first demonstrated the highly polymorphic nature of SSRs in 1989. In a $(TG)_n$ repeat in the human cardiac muscle actin gene locus, Litt and Luty (1989) detected 12 length variants (alleles) in only 37 individuals. Likewise, Weber and May (1989) reported successful amplification of products from 10 dinucleotide SSR loci and found from 4 to 11 alleles at each by typing a maximum of 78 individuals. Numerous reports support the high frequency of polymorphic SSR loci in the human genome. It is also important to note that SSR loci appear to be randomly spaced throughout the human genome (Hamada et al. 1982; Stallings et al. 1990). As defined by Edwards et al. (1991), SSR loci include tri- and tetrameric repeats such as $(AAT)_n$ and $(AGAT)_n$, respectively. According to these authors, the combined frequency in the human genome of all 44 possible unique tri- and tetrameric SSRs with n = 7 or greater is estimated to be 400,000 or one SSR per 10 kbp. If even a small fraction of these loci were polymorphic, they would provide ample markers for a saturated genetic map.

SSR Loci in DNA Fingerprinting

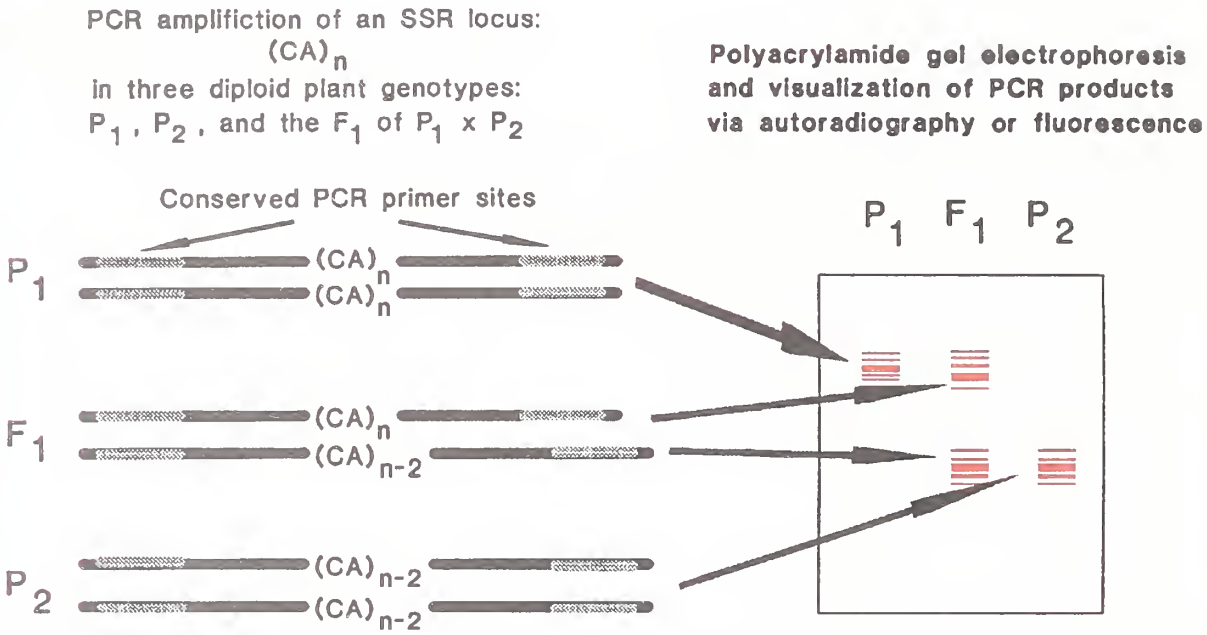
SSR markers can be employed in the development of unique allelic profiles for establishing individual identity. Distinctive profiles can be readily generated by defining the allelic constitution of individuals at relatively few loci, each of which is multi-allelic. Such a system is open-ended in that additional loci can be added if those already in use are inadequate to produce a unique profile for all individuals. With the advent of the Plant Variety Protection Act such a definitive cultivar identification system would be extremely useful.

Do SSRs Occur in Plants?

Can SSRs be used in plant genetic studies? Of particular interest in this regard is the occurence of SSR DNA in higher plants. Tautz et al. (1986) examined the European Molecular Biology Laboratory DNA sequence library for the presence of di- and trinucleotide repeats. A comparison of very limited plant and algal sequence data with those of vertebrates indicated a similar frequency of the two types of SSR's in the two groups of organisms.

Sarkar et al. (1991) reported a search of GenBank™ sequences for purine/pyrimidine repeats greater than 13 units in length. Calculations from their data indicate 2.3 such SSR

Figure 1. Generation and visualization of Simple Sequence Repeat Length Polymorphism.



loci per 100 kb in primates and 1.8 in yeast. While these reports are not clearly indicative of SSR's in higher plants, they do suggest the possibility of their occurrence. The only published report clearly documenting SSR's in higher plants is that of Condit and Hubbell (1991). They screened DNA libraries of five tropical tree species as well as *Zea mays* for the presence of clones containing $(AC)_n$ and $(AG)_n$ repeat sequences. They estimated a total of $(AC)_n + (AG)_n$ SSR sequences ranging from 5×10^3 to 3 to 10^5 among six species examined.

It seemed appropriate to undertake a further investigation of SSR DNA in plant genomes. Therefore, a search of GenBank™ was completed with the assistance of Dr. Susan McCarthy, Coordinator for the National Agricultural Library Plant Genome Data and Information Center. Despite the limited number of plant sequences available in GenBank™, a number of di- and tri-nucleotide SSR's were identified (Table 1). The data support the presence of SSR DNA in numerous plant species, including crop plants.

Do Plant SSR's Exhibit Length Polymorphism?

At this time no published information is available to answer this question. However, Weber (1990) suggested that human $(CA)_n$ sequences with n of 10 or less are unlikely to exhibit length polymorphism, whereas sequences with n greater than 15 are consistently polymorphic.

A more detailed look at the data obtained from the search of GenBank™, reported in Table 1, indicates at least one instance of a SSR with greater than 15 tandem repeats in each of the following higher plant species: *Arabidopsis thanliana, Daucus carota, Glycine max, Hordeum vulgare, Nicotiana tabacum, Pisum sativum, Oryza sativa, Solanum tuberosum,* and *Zea mays*. This finding suggests that plant SSR's have a high probability of exhibiting length polymorphism.

Technical Questions

One obvious drawback to developing a genetic linkage map generated using SSR markers is the time-consuming nature of the steps required to identify polymorphic loci. This is particularly true of SSR

Table 1. The number and average distance (in kilobase pairs) between all possible dimeric, trimeric, and tetrameric Simple Sequence Repeat DNA sequences in plant species determined from a search of GenBank™.

Plant species	Kilobases searched kbp	Dimeric repeats* No.	Dimeric repeats* Distance between repeats kbp	Trimeric repeats† No.	Trimeric repeats† Distance between repeats kbp	Tetrameric repeats‡ No.	Tetrameric repeats‡ Distance between repeats kbp
Saccharomyces cervisiae	2288	40	57	29	79	2	1144
Nicotiana tabacum	118	4	29	0	-	0	-
Glycine max	212	6	35	1	212	4	53
Lycopersicon esculentum	135	2	68	0	-	1	135
Triticum aestivum	151	1	151	43	4	0	-
Medicago sativa	30	0	-	1	30	0	-
Pisum sativum	129	3	43	3	43	2	64
Zea mays	368	3	123	4	91	6	61
Arabidopsis thaliana	247	4	62	1	247	0	-
Oryza sativa	137	2	68	2	68	6	23

* Dimeric repeats such as $(AT)_n$ with n > 9.
† Trimeric repeats such as $(ATT)_n$ with n > 7.
‡ Tetrameric repeats such as $(AGAT)_n$ with n > 4.

markers as compared with the RAPD system. First, a DNA library must be developed and screened with a repetitive sequence oligonucleotide probe to identify desired clones. If the library is composed of relatively short clones, selected clones can be sequenced in their entirety to identify the SSR and determine flanking sequences. If the library is composed of longer sequences, subcloning and identification of the appropriate subclone would be required before sequencing. To expedite SSR isolation and sequencing, at least two PCR-assisted procedures have been suggested. Edwards et al. (1991) proposed a protocol that allows the amplification of the subclone containing the SSR followed by sequencing of flanking DNA regions. Browne and Litt (1992) suggested the use of a set of degenerate sequencing primers that anneal directly to the SSR. Both procedures should allow relatively rapid determination of sequences flanking SSR's and thereby expedite PCR primer selection.

A second possible impediment to the widespread use of SSR length polymorphisms by plant geneticists may be the perception that the routine detection of PCR products differing only slightly in length is difficult and laborious. Much of the work reported to date with SSR makers has used ^{32}P labeled PCR products and denaturing polyacrylamide gels. The use of fluorescent dye labeled PCR primers and fluorescent detection of multiplex PCR products (Edwards et al., 1991) offers the prospect of rapid determination of the allelic constitution of three SSR loci from one PCR reaction.

A less costly approach, but one that may be quite functional, would be the use of non-denaturing polyacrylamide gel separation followed by ethidium bromide or silver staining. The elimination of secondary structure via denaturation may not be necessary for distinguishing DNA fragments that only vary in composition by the presence or absence of a few internal SSR units.

Many technical questions remain as to the applicability and use of polymorphic SSR sequences in plant genetic studies. However, the informativeness of this type of marker, the rapid detection via PCR, and the potential of tens of thousands of SSR sequences per genome suggest that plant geneticists may wish to consider the use of polymorphic SSR loci as genetic markers. Genetic markers generated via variation in SSR length may provide a useful complement to the RFLP and RAPD markers currently in use.

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CURD — continued from page 16

among experts, co-sponsors, and problem areas.

Availability

CURD is available online to anyone using a microcomputer and modem. After allowing users one free search, KSU charges a fee per online session. Individuals seeking access may contact the CURD office at the following address:

Corn Utilization Research Database
Food and Feed Grains Institute
Farrell Library, Room 419
Kansas State University
Manhattan, KS 66506-1200
Ph (913) 532-7452; FAX (913) 532-5861
INTERNET:
CURD@KSUVM.KSU.EDU ◆

Hard Copy

Improving End-User Computer Searches

Vincent Caccese, Librarian
Biological & Agricultural Sciences Reference Department
Shields Library
University of California, Davis, CA

Since their appearance in the early 1970's, computerized databases have been a boon to the searching of scientific literature. Increasing numbers of end-users conduct their own computer searches without direct assistance of an intermediary. They are generally satisfied with the results. For individuals less pleased with their searching skills, the following suggestions may prove helpful.

Principles of Searching

Many texts are available that explain the principles of searching.[1] In brief, users can improve search results if they can determine (1) the scope of the database being used, dates of coverage, and the frequency of its update; (2) the database producer's policy of selecting source publications and the extent to which those publications are indexed selectively or cover to cover; (3) the correct format of an author's name being searched; (4) the system default for a Boolean operator when none is entered between terms by the user; (5) the optimal number of concepts to intersect with AND; and (6) whether controlled search terms or codes are used.

A good database manual will address the above points and clarify whether or not a database is appropriate for a given question. If a manual is not available or is incomplete, the convenient but less exhaustive alternatives are the help screens in CD-ROM systems. These provide summary statements about the database and time periods covered. Other excellent sources are the data sheets from online vendors that describe the databases available through them. Online systems also have limited help screens associated with a particular database as well as directory files online devoted to database descriptions.[2] Because of per minute costs, these can be expensive. Several other print database directories give additional guidance on database coverage and are available in larger libraries.[3]

Scope and Coverage

After selecting the likely databases to use, determine the scope and depth of coverage. Periodicals are generally the largest component of scientific bibliographic databases. A database "list of periodicals indexed" can be an aid to the database manual in assessing source publication coverage. However, few databases attempt to represent the contents of periodicals cover to cover; fewer still will index to the depth expected by any given user. In general, news items, letters, book reviews, and shorter communications are commonly excluded. Dissertations, patents, and books are covered unevenly among databases.

Databases also vary in the degree of currency of its records compared with the dates of the source publications. Because of the labor-intensive nature of indexing, it is not unusual for the online database to contain a reference to a source publication 3 months behind the date of the original. This potentially long delay should alert the user not to rely solely on one or even two databases for literature coverage.

Author names, in particular, are troublesome for searching. There is a deception that they are easy to search. The authors themselves are inconsistent in how they present their names.

In addition, each database has unique formatting requirements. The rule of thumb is always examine the index or expand features in online and CD-ROM systems for author format. If the format varies even slightly from what the user entered, it pays to re-enter the name and search again.

Searching Approach

Conceptualizing a search beforehand is a good practice. A common and effective approach for the user is to divide a question into concepts — two or three in most cases in bibliographic text files. How a user dissects a topic is related to a number of factors, including individual needs, subject expertise, and the database itself. The greater the number of concepts to intersect by AND, the more likely the results will tend toward zero. The simple technique of removing a concept requirement provides an option for recalling greater results.

The user lists for each concept the terms, synonyms, near synonyms, antonyms, and any codes assigned by the database to represent any concepts. The terms in each conceptual grouping will be joined by the union operator OR and the result intersected with the remaining concepts by means of other logical operators such as AND or NOT. Many database systems operate on terms immediately connected by AND, and then by OR. For this reason, these operators have to be diligently separated, either by nesting of any like terms that are ORed, or by creating separate sets for each concept before ANDing with another. The user also should be aware of any logical operators supplied by default by the software.

Selecting Entry Terms

When given a choice, users commonly search for title words. Title words in a database originate, at the very least, in the title provided by the author and from words that might be added by the indexer.

Any one database might stop with the recording of title words only. Other databases reflect a continuum of additional search points. For example, there may be other subject-like words sometimes called "identifiers," which include new jargon or other kinds of terms not under standardized control.

At the other end of the continuum are database-controlled terms, which include hierarchies and standardized language preferred by the database to express alternate words or concepts. The only sure way to determine whether the database is using controlled terms for searching is to consult the database description mentioned earlier.

Good databases have various search aids for user guidance, including thesauri, hierarchical structures, lists of reference works used as authorities, and the previously mentioned lists of periodicals indexed.

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3. *Information Industry Directory*, 12th edition. Detroit: Gale Research, Inc., 1992. 2 vols. Reviews of recent directories have appeared in *Information Intelligence Online Newsletter*. 13(2):10-13, February 1992.

Top Ten Databases

On-line databases were searched to find the files with the most citations for genetic, chromosomal, or linkage mapping. All of these databases are commercially available through Dialog.

1 EMBASE (Excerpta Medica) 1974-92
2 BIOSIS (Biological Abstracts) 1969-92
3 PASCAL (English/French) 1973-1992
4 CA SEARCH (Chemical Abstracts) 1967-92
5 SCISEARCH (Science Citation Index) 1974-92
6 LIFE SCIENCES COLLECTION 1978-92
7 CAB ABSTRACTS (Agricultural and Biological) 1972-92
8 AGRICOLA (Agri/Bio) 1979-92
9 BIOTECHNOLOGY ABSTRACTS 1982-92
10 SUPERTECH (Biotech/computer) 1973-92

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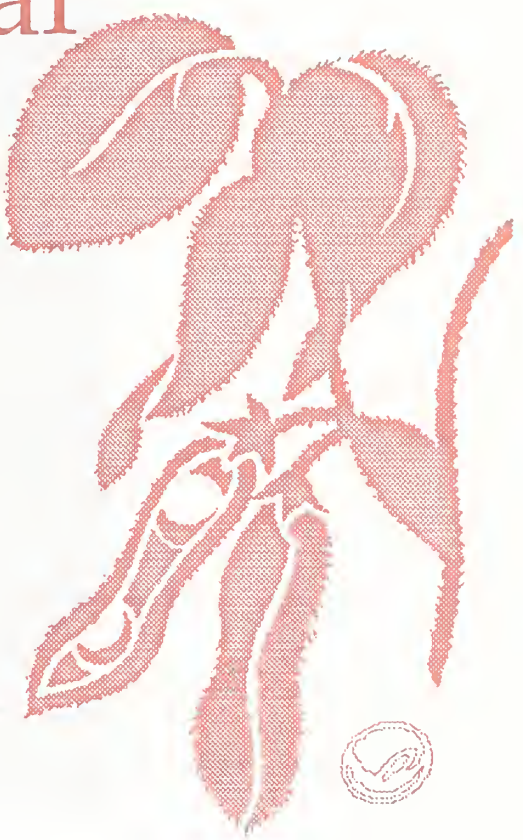

Topics:

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Where: Scheman Building
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Ames Iowa

When: July 27-29, 1992

Registration: Registration fee for the conference is $45 for students and $70 for non-students. Registration deadline is July 17, 1992. After the deadline, add $10 to the registration fee.

For more information or to request a brochure contact:
Janet Gardner, Iowa State University, Continuing Education, 102 Scheman Building, Ames, Iowa 50011-1112
Telephone (515) 294-5366

Transportation: Iowa State University is located 50 kilometers from Des Moines International Airport which is served by several major carriers. Rental cars are available at the airport. Shuttle service will be provided to and from the meeting site in Ames, since bus services is very limited.

On the Horizon

Calendar of Upcoming Genome Events

MEETINGS - 1992

July 5-10: **Yeast Chromosome Structure, Replication and Segregation,** Snowmass, CO. Contact: FASEB Summer Research Conference Office, 9650 Rockville, Pike, Bethesda, MD 20814-3998. FAX: (301) 530-7014.

July 13-17: **Gordon Research Conference, Molecular Genetics,** Newport, RI. Contact: Dr. Alexander M. Cruickshank, Gordon Research Center, University of Rhode Island, Kingston, RI 02881-0801. Telephone: (401) 783-4011 or (401) 783-3372, FAX: (401) 783-7644.

July 14-22: **1st International Crop Science Congress,** Ames, IA. Contact: Kenneth Frey, Chair, International Crop Science Congress, c/o Agronomy Dept., Iowa State University, Ames, IA 50011.

July 21-25: **Science Innovation '92: New Techniques and Instruments in Biomedical Research,** San Francisco, CA. Contact: AAAS Meetings Office, 1333 H St. NW, Washington, DC 20005. Telephone: (202) 326-6450, FAX: (202) 289-4021.

July 27-28: **Mid-Atlantic Plant Molecular Biology Society Ninth Annual Meeting,** Beltsville, MD. Contact: Frank Turano, USDA/ARS, Climate Stress Laboratory, Bldg. 001, Rm. 206, BARC-West, Beltsville, MD 20705. Telephone: (301) 504-6145, FAX: (301) 504-7521.

July 27-29: **4th Biennial Conference on Molecular and Cellular Biology of the Soybean,** Ames, IA. Contact: Mary Ann Simpson, Marketing and Conference Coordinator, 1209 Friley Hall, Iowa State University, Ames, IA 50012. Telephone: (515) 294-8384, FAX: (515) 294-0967.

July 27-31: **Gordon Research Conference, Nuclear Proteins, Gene Regulation & Chromatin Structure,** Tilton, NH. Contact: Dr. Alexander M. Cruickshank, Gordon Research Center, University of Rhode Island, Kingston, RI 02881-0801. Telephone: (401) 783-4011 or (401) 783-3372, FAX: (401) 783-7644.

August 1-5: **1992 Annual Meeting of the American Society of Plant Physiologists,** Pittsburgh, PA. Contact: ASPP, 15501 Monona Drive, Rockville, MD 20855-2768. Telephone: (301) 251-2651, FAX: (301) 279-2996.

August 3-14: **Post-Transcriptional Control of Gene Expression,** Spetsai, Greece. Contact: Prof. A. Von Gabain, Karolinska Institute, Box 60400, S-104 01 Stockholm, Sweden.

August 4-8: **11th International Chromosome Conference,** Edinburgh, UK. Contact: Dr. Ann Chandley, MRC Human Genetics Unit, Western General Hospital, Edinburgh EH4 2XU, United Kingdom.

August 9-14: **Plant Molecular Genetics,** Copper Mountain. Contact: ASEB Summer Research Conference Office, 9650 Rockville Pike, Bethesda, MD 20814-3998. FAX: (301) 530-7014.

August 10-14: **Biotechnology: Principles and Processes.** Contact: Director of Summer Session, MIT, Room E19-356, Cambridge, MA 02139.

August 15-21: **16th International Conference on Yeast Genetics and Molecular Biology,** Vienna, Austria. Contact: Interconvention Austria Center Vienna, A-1450 Vienna, Austria.

August 15-21: **XVIIth International Genetics Congress,** Birmingham, UK. Contact: Dr. J.P.W. Young, John Innes Institute, Colney Lane, Norwich NR4 7JH.

August 16-21: **9th International Biotechnology Symposium and Exposition, Harnessing Biotechnology for the 21st Century,** Crystal City, VA. Contact: American Chemical Society, 1155 Sixteenth Street, NW, Room 205, Washington, DC 20036. Telephone: (202) 872-4485, FAX: (202) 872-6067.

August 18-21: **Plant Biotechnology Methods.** Contact: Bioprocessing Resource Center, Pennsylvania State University, 519 Waartik Lab, University Park, PA 16801-9959. Telephone: (800) 833-5533 or (814) 863-3650.

August 20-23: **First European Conference on Fungal Genetics,** Nottingham, UK. Contact: Prof. J.F. Peberdy, ECFG 1 Secretariat, Dept. of Botany, University of Nottingham, Nottingham NG7 2RD, UK.

August 23-28: **8th International Symposium on Yeasts,** Atlanta, GA. Contact: Dr. S.A. Meyer, Dept. of Biology, Georgia State University, P.O. Box 4010, Atlanta, GA 30302.

August 24-28: **International Symposium on Population Genetics and Gene Conservation of Forest Trees,** Bordeaux, France. Contact: P.H. Baradat, INRA, B.P. 45 33511, Gazinet Cedex, France. Telephone: 33-56-68-03-13. FAX: 33-56-68-02-23.

August 30-September 4: **9th International Congress on Photosynthesis,** Nagoya, Japan. Contact: Prof. Norio Murata, Secretariat, 9th International Congress on Photosynthesis, National Institute for Basic Biology, Okazaki 444, Japan.

August 31-September 10: **Mechanisms in Eukaryotic Gene Regulation,** Spetsai, Greece. Contact: Prof. H. Feldmann, Universitat Munchen, Institut fur Physiologische Chemie, Schillerstrasse 44, D-8000 Munchen 2, Germany.

September 1-12: **Tyrosine Phosphorylation/Dephosphorylation and Downstream Signaling,** Maratea, Italy. Contact: Prof. L.M.G. Heilmeyer, Ruhr-Universitat Bochum, Institut fur Physiologische Chemie, Universitatsstrasse 150, D-4630 Bochum 1, Germany.

September 6-18: **Approaches to Molecular Biology of In Vitro Plant Morphogenesis,** Crete, Greece. Contact: Dr. K.A. Roubelakis-Angelakis, University of Crete, Dept. of Biology, P.O. Box 1470, 71110 Heraklion, Greece.

September 12-18: **Genome Organization, Function and Evolution,** Septsai, Greece. Contact: Dr. G. Bernardi, CNRS, Institut Jacques Monod. Lab. de Genetique Moleculaire, 2 Place Jussieu, Tour 43, 75005 Paris, France.

September 13-16: **Molecular Biology of Mitochondrial Transport Systems,** Rosa Marina, Italy. Contact: Dr. M. Forte, Oregon Health Sciences University, Vollum Institute, 3181 S.W. Sam Jackson Park Road, Portland, OR 97201-3098.

September 14-15: **BioFinance/BioPartnering '92,** New York, NY. Telephone: (212) 996-5679, FAX: (212) 996-1444.

September 26-30: **Genome Sequencing and Analysis Conference IV,** Hilton Head, SC Contact: Susan Wallace, P.O. Box 541, Rockville, MD 20848. Telephone: (301) 480-0634, FAX: (301) 480-8588.

November 7-11: **Program In Mathematics and Molecular Biology III: Computational Approaches to Nucleic Acid Structure and Function,** Sante Fe, NM. Contact: Dr. S.J. Spengler, Math. & Molecular Biology, 103 Donner Laboratory, University of California, Berkeley, CA 94720. FAX: (510) 642-4071.

November 8-11: **2nd International Conference on DNA Fingerprinting,** Belo Horizonte, Brazil. Contact: Prof. Sergio D.J. Pena, Nucleo de Genetica Medica de Minas Gerais, Avenida Afonso Pena, 3111-9 Andar, Caixa Postal 3396, CEP 30112, Belo Horizonte, MG, Brazil.

November 9-11: **Plant Genome I,** San Diego, CA. Contact: Scherago International, Inc., 11 Penn Plaza, Ste 1003, New York, NY 10001. Telephone: (212) 643-1750, FAX: (212) 643-1758.

Workshops and Courses - 1992

July 6-10: **DNA-Binding Proteins and Transcriptional Regulators,** Course 119-92, Washington, DC. Contact: Center for Advanced Training in Cell and Molecular Biology, Catholic University of America, Washington, DC 20064. Telephone: (202) 319-6161, FAX: (202) 319-4467 or (202) 319-5721.

July 13-17: **Protein and Nucleic Acid Separation Techniques,** Course 120-92, Washington, DC. Contact: Center for

Advanced Training in Cell and Molecular Biology, Catholic University of America, Washington, DC 20064. Telephone: (202) 319-6161, FAX: (202) 319-4467 or (202) 319-5721.

July 21-August 10: **Advanced Molecular Cloning & Expression of Eukaryotic Genes,** Cold Spring Harbor, NY. Contact: Meetings Office, Cold Spring Harbor Laboratory, 1 Bungtown Rd., P.O. Box 100, Cold Spring Harbor, NY. Telephone: (516) 367-8346.

July 21-August 10: **Yeast Genetics,** Cold Spring Harbor, NY. Contact: Meetings Office, Cold Spring Harbor Laboratory, 1 Bungtown Rd., P.O. Box 100, Cold Spring Harbor, NY. Telephone: (516) 367-8346.

September 14-17: **PCR Methodology Workshop,** Columbia, MD. Contact: Workshop Coordinator, Exon-Intron, Inc., 9151 Rumsey Rd., Suite 130, Columbia, MD 21045-1929. Telephone: (301) 730-3984.

September 23-25: **Genome Mapping of Wheat and Related Species, Third Annual International Public Workshop,** CIMMYT Headquarters, Mexico. Contact: Dr. David Hoisington, CIMMYT, Lisboa 27, Apdo. Postal 6-641, 06600 Mexico, DF Mexico. Telephone: Ms. S. Velazquez 5-25-954-2100 ext. 1382, FAX: 5-25-954-1069.

Future Events

January 9-15, 1993: **Keystone Symposia on Molecular & Cellular Biology: The Extracellular Matrix of Plants: Molecular, Cellular and Developmental Biology,** Santa Fe, NM. Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. Telephone: (303) 262-1230.

January 17-22, 1993: **Miami Bio/Technology Winter Symposia, Advances in Gene Technology: Protein Engineering and Beyond,** Miami, FL. Contact: Sandra Black, P.O. Box 016129, Miami, FL 33101. Telephone: (800) 642-4363, FAX: (305) 324-5665.

January 26-February 1, 1993: **Keystone Symposia on Molecular & Cellular Biology: Evolution and Plant Development,** Taos, NM. Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. Telephone: (303) 262-1230.

February 8-14, 1993: **Keystone Symposia on Molecular & Cellular Biology: Genetic and In Vitro Analysis of Cell compartmentalization,** Taos, NM. Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. Telephone: (303) 262-1230.

February 23-March 1, 1993: **Keystone Symposia on Molecular & Cellular Biology: Nucleases: Structure, Function and Biological Roles,** Tamarron, CO. Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. Telephone: (303) 262-1230.

March 7-14, 1993: **Keystone Symposia on Molecular & Cellular Biology: Frontiers of NMR in Molecular Biology-III,** Taos, NM. Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. Telephone: (303) 262-1230.

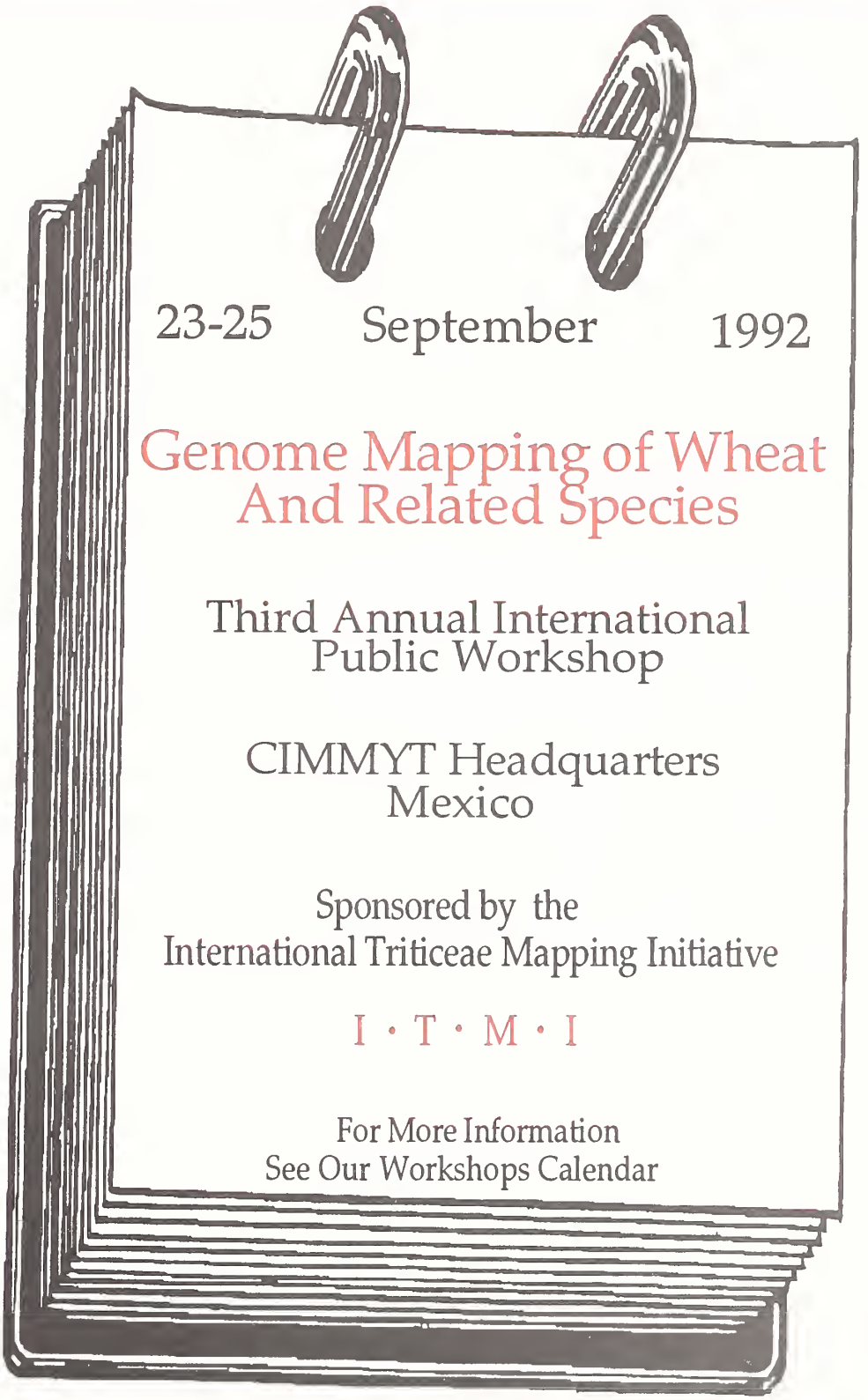
March 31-April 3, 1993: **Twelfth Annual Symposium: Current Topics in Plant Biochemistry, Molecular Biology and Physiology,** Columbia, MO. Contact: Doug Randall, 117 Schweitzer Hall, University of Missouri-Columbia, Columbia, MO 65211. Telephone: (314) 882-7796, FAX: (314) 882-5635.

April 18-25, 1993: **Keystone Symposia on Molecular & Cellular Biology: Transposition and Site-Specific Recombination: Mechanism and Biology,** Keystone, CO. Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. Telephone: (303) 262-1230.

April 21-25, 1993: **Molecular Genetics of Plant-Microbe Interactions (Workshop and Symposia),** East Brunswick, NJ. Contact: Rutgers, State University of New Jersey, Registration Desk, Office of Continuing Professional Education, Cook College, P.O. Box 231, New Brunswick, NJ 08903. Telephone: (908) 932-9271, FAX: (908) 932-8726.

May 8-13, 1994: **HPLC'94, Eighteenth International Symposium on High Performance Liquid Chromatography,** Minneapolis, MN. Contact: Barr Enterprises, P.O. Box 279, Walkerville, MD. Telephone: (301) 898-3772, FAX: (301) 898-5596.

June 16-21, 1996: **HPLC'96, Twentieth International Symposium on High Performance Liquid Chromatography,** San Francisco, CA. Contact: Barr Enterprises, P.O. Box 279, Walkerville, MD. Telephone: (301) 898-3772, FAX: (301) 898-5596.



23-25 September 1992

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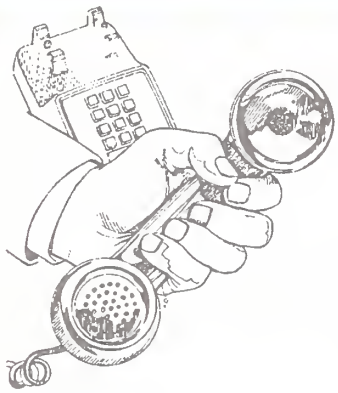

Introducing Dr. George Jen

Dr. George Jen is the new Plant Genome Program Director for the National Research Initiative Competitive Grants Program. The position is in USDA's Cooperative State Research Service, Office of Grants and Program Systems. Dr. Jen provides leadership and direction in awarding competitive grants to U.S. scientists for plant genome research projects.

Dr. Jen's background includes broad experience in biotechnology, and training in the areas of molecular biology, virology, and bacterial genetics.

Before coming to USDA in February, Dr. Jen held the position of senior scientist at CIBA-Geigy's Agricultural Biotechnology Research Unit in North Carolina. From 1985 to 1991, he worked on new strategies and methods for plant gene expression and transformation; studied the nuclear uptake of DNA in animal and plant cells; determined the fine-structure of insert DNA in transgenic plants; developed an *Arabidopsis* molecular genetics program; and implemented a genetic-engineering program for developing herbicide-resistant plants.

Prior to graduate school, Dr. Jen was a senior research associate with the Cetus Corporation in Berkeley, California.There he studied the biochemistry and physiology of antibiotic biosynthesis in *Actinomyces*.

Dr. Jen holds a Ph.D. in molecular biology from Washington University in St. Louis, Missouri. His studies dealt with translational regulation in virus-infected animal cells. Dr. Jen also completed post-graduate work there as an NIH Postdoctoral Fellow, from 1982-1985, in the laboratory of Dr. Mary-Dell Chilton. His research included the study of the *Agrobacterium tumefacien* transformation of plant cells. Dr. Jen completed his undergraduate studies at the University of California-Berkeley, where he majored in biochemistry and bacteriology.

He has authored and coauthored numerous articles for scientific journals and proceedings, and has served as a reviewer of various publications.

Dr. Jen is able to answer questions about the USDA Plant Genome Competitive Grants Program. He can be reached at (202) 401-5022

Probe

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